

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/727,358 B
Source: IFW16
Date Processed by STIC: 10/19/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 10/19/2006

PATENT APPLICATION: US/10/727,358B

TIME: 08:17:35

Input Set : A:\1216-1-006CIPSEQLISTREV10.06.TXT

Output Set: N:\CRF4\10192006\J727358B.raw

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4 <110> APPLICANT: Kolesnick, Richard N.
5   Xing, Hong-Mei R.
7 <120> TITLE OF INVENTION: Kinase Suppressor of Ras Inactivation
8   for Therapy of Ras Mediated Tumorigenesis
11 <130> FILE REFERENCE: 1216-1-006CIP
13 <140> CURRENT APPLICATION NUMBER: 10/727,358B
14 <141> CURRENT FILING DATE: 2003-12-03
16 <150> PRIOR APPLICATION NUMBER: 60/384,228
17 <151> PRIOR FILING DATE: 2002-05-30
19 <150> PRIOR APPLICATION NUMBER: 60/460,023
20 <151> PRIOR FILING DATE: 2003-04-03
22 <150> PRIOR APPLICATION NUMBER: PCT/US03/16961
23 <151> PRIOR FILING DATE: 2003-05-29
25 <160> NUMBER OF SEQ ID NOS: 56
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 120
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <400> SEQUENCE: 1
35 ctgcagaagc tcatcgatat ctccatcggc agtctgcgcg ggctgcgcac caagtgtctca 60
36 gtgtctaacg acctcacaca gcaggagatc cggaccctag aggcaaagct ggtgaaatac 120
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 41
41 <212> TYPE: PRT
42 <213> ORGANISM: Homo sapiens
44 <400> SEQUENCE: 2
45 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
46 1           5           10           15
47 Thr Lys Cys Ser Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
48           20           25           30
49 Leu Glu Ala Lys Leu Val Lys Tyr Ile
50           35           40
53 <210> SEQ ID NO: 3
54 <211> LENGTH: 19
55 <212> TYPE: DNA
56 <213> ORGANISM: Homo sapiens
58 <400> SEQUENCE: 3
59 ggcagtctgc gcgggctgc
61 <210> SEQ ID NO: 4
62 <211> LENGTH: 18
63 <212> TYPE: DNA
64 <213> ORGANISM: Homo sapiens

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66 <400> SEQUENCE: 4
67 tcagtgtcta acgacctc                                     18
69 <210> SEQ ID NO: 5
70 <211> LENGTH: 18
71 <212> TYPE: DNA
72 <213> ORGANISM: Homo sapiens
74 <400> SEQUENCE: 5
75 cggaccctag aggcaaag                                     18
77 <210> SEQ ID NO: 6
78 <211> LENGTH: 19
79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: antisense oligonucleotide
85 <400> SEQUENCE: 6
86 cagcccgcgcg agactgccg                                     19
88 <210> SEQ ID NO: 7
89 <211> LENGTH: 18
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: antisense oligonucleotide
96 <400> SEQUENCE: 7
97 gaggtcggtta gacactga                                     18
99 <210> SEQ ID NO: 8
100 <211> LENGTH: 16
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: antisense oligonucleotide
107 <400> SEQUENCE: 8
108 ctttgccctct agggtc                                     16
110 <210> SEQ ID NO: 9
111 <211> LENGTH: 873
112 <212> TYPE: PRT
113 <213> ORGANISM: Mus musculus
115 <400> SEQUENCE: 9
116 Met Asp Arg Ala Ala Leu Arg Ala Ala Ala Met Gly Glu Lys Lys Glu
117 1          5          10          15
118 Gly Gly Gly Gly Gly Ala Ala Ala Asp Gly Gly Ala Gly Ala Ala Val
119          20          25          30
120 Ser Arg Ala Leu Gln Gln Cys Gly Gln Leu Gln Lys Leu Ile Asp Ile
121          35          40          45
122 Ser Ile Gly Ser Leu Arg Gly Leu Arg Thr Lys Cys Ser Val Ser Asn
123          50          55          60
124 Asp Leu Thr Gln Gln Glu Ile Arg Thr Leu Glu Ala Lys Leu Val Lys
125 65          70          75          80
126 Tyr Ile Cys Lys Gln Gln Gln Ser Lys Leu Ser Val Thr Pro Ser Asp
127          85          90          95

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128 Arg Thr Ala Glu Leu Asn Ser Tyr Pro Arg Phe Ser Asp Trp Leu Tyr
129          100          105          110
130 Ile Phe Asn Val Arg Pro Glu Val Val Gln Glu Ile Pro Gln Glu Leu
131          115          120          125
132 Thr Leu Asp Ala Leu Leu Glu Met Asp Glu Ala Lys Ala Lys Glu Met
133          130          135          140
134 Leu Arg Arg Trp Gly Ala Ser Thr Glu Glu Cys Ser Arg Leu Gln Gln
135 145          150          155          160
136 Ala Leu Thr Cys Leu Arg Lys Val Thr Gly Leu Gly Gly Glu His Lys
137          165          170          175
138 Met Asp Ser Gly Trp Ser Ser Thr Asp Ala Arg Asp Ser Ser Leu Gly
139          180          185          190
140 Pro Pro Met Asp Met Leu Ser Ser Leu Gly Arg Ala Gly Ala Ser Thr
141          195          200          205
142 Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala Ser Asp Ser
143          210          215          220
144 Pro Val Pro Gly Leu Ser Glu Gly Leu Ser Asp Ser Cys Ile Pro Leu
145 225          230          235          240
146 His Thr Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser Phe Ile Thr
147          245          250          255
148 Pro Pro Thr Thr Pro Gln Leu Arg Arg His Ala Lys Leu Lys Pro Pro
149          260          265          270
150 Arg Thr Pro Pro Pro Pro Ser Arg Lys Val Phe Gln Leu Leu Pro Ser
151          275          280          285
152 Phe Pro Thr Leu Thr Arg Ser Lys Ser His Glu Ser Gln Leu Gly Asn
153          290          295          300
154 Arg Ile Asp Asp Val Thr Pro Met Lys Phe Glu Leu Pro His Gly Ser
155 305          310          315          320
156 Pro Gln Leu Val Arg Arg Asp Ile Gly Leu Ser Val Thr His Arg Phe
157          325          330          335
158 Ser Thr Lys Ser Trp Leu Ser Gln Val Cys Asn Val Cys Gln Lys Ser
159          340          345          350
160 Met Ile Phe Gly Val Lys Cys Lys His Cys Arg Leu Lys Cys His Asn
161          355          360          365
162 Lys Cys Thr Lys Glu Ala Pro Ala Cys Arg Ile Thr Phe Leu Pro Leu
163          370          375          380
164 Ala Arg Leu Arg Arg Thr Glu Ser Val Pro Ser Asp Ile Asn Asn Pro
165 385          390          395          400
166 Val Asp Arg Ala Ala Glu Pro His Phe Gly Thr Leu Pro Lys Ala Leu
167          405          410          415
168 Thr Lys Lys Glu His Pro Pro Ala Met Asn Leu Asp Ser Ser Ser Asn
169          420          425          430
170 Pro Ser Ser Thr Thr Ser Ser Thr Pro Ser Ser Pro Ala Pro Phe Leu
171          435          440          445
172 Thr Ser Ser Asn Pro Ser Ser Ala Thr Thr Pro Pro Asn Pro Ser Pro
173          450          455          460
174 Gly Gln Arg Asp Ser Arg Phe Ser Phe Pro Asp Ile Ser Ala Cys Ser
175 465          470          475          480
176 Gln Ala Ala Pro Leu Ser Ser Thr Ala Asp Ser Thr Arg Leu Asp Asp

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177          485          490          495
178 Gln Pro Lys Thr Asp Val Leu Gly Val His Glu Ala Glu Ala Glu Glu
179          500          505          510
180 Pro Glu Ala Gly Lys Ser Glu Ala Glu Asp Asp Glu Glu Asp Glu Val
181          515          520          525
182 Asp Asp Leu Pro Ser Ser Arg Arg Pro Trp Arg Gly Pro Ile Ser Arg
183          530          535          540
184 Lys Ala Ser Gln Thr Ser Val Tyr Leu Gln Glu Trp Asp Ile Pro Phe
185 545          550          555          560
186 Glu Gln Val Glu Leu Gly Glu Pro Ile Gly Gln Gly Arg Trp Gly Arg
187          565          570          575
188 Val His Arg Gly Arg Trp His Gly Glu Val Ala Ile Arg Leu Leu Glu
189          580          585          590
190 Met Asp Gly His Asn Gln Asp His Leu Lys Leu Phe Lys Lys Glu Val
191          595          600          605
192 Met Asn Tyr Arg Gln Thr Arg His Glu Asn Val Val Leu Phe Met Gly
193          610          615          620
194 Ala Cys Met Asn Pro Pro His Leu Ala Ile Ile Thr Ser Phe Cys Lys
195 625          630          635          640
196 Gly Arg Thr Leu His Ser Phe Val Arg Asp Pro Lys Thr Ser Leu Asp
197          645          650          655
198 Ile Asn Lys Thr Arg Gln Ile Ala Gln Glu Ile Ile Lys Gly Met Gly
199          660          665          670
200 Tyr Leu His Ala Lys Gly Ile Val His Lys Asp Leu Lys Ser Lys Asn
201          675          680          685
202 Val Phe Tyr Asp Asn Gly Lys Val Val Ile Thr Asp Phe Gly Leu Phe
203          690          695          700
204 Gly Ile Ser Gly Val Val Arg Glu Glu Arg Arg Glu Asn Gln Leu Lys
205 705          710          715          720
206 Leu Ser His Asp Trp Leu Cys Tyr Leu Ala Pro Glu Ile Val Arg Glu
207          725          730          735
208 Met Ile Pro Gly Arg Asp Glu Asp Gln Leu Pro Phe Ser Lys Ala Ala
209          740          745          750
210 Asp Val Tyr Ala Phe Gly Thr Val Trp Tyr Glu Leu Gln Ala Arg Asp
211          755          760          765
212 Trp Pro Phe Lys His Gln Pro Ala Glu Ala Leu Ile Trp Gln Ile Gly
213          770          775          780
214 Ser Gly Glu Gly Val Arg Arg Val Leu Ala Ser Val Ser Leu Gly Lys
215 785          790          795          800
216 Glu Val Gly Glu Ile Leu Ser Ala Cys Trp Ala Phe Asp Leu Gln Glu
217          805          810          815
218 Arg Pro Ser Phe Ser Leu Leu Met Asp Met Leu Glu Arg Leu Pro Lys
219          820          825          830
220 Leu Asn Arg Arg Leu Ser His Pro Gly His Phe Trp Lys Ser Ala Asp
221          835          840          845
222 Ile Asn Ser Ser Lys Val Met Pro Arg Phe Glu Arg Phe Gly Leu Gly
223          850          855          860
224 Thr Leu Glu Ser Gly Asn Pro Lys Met
225 865          870

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228 <210> SEQ ID NO: 10
229 <211> LENGTH: 866
230 <212> TYPE: PRT
231 <213> ORGANISM: Homo sapiens
233 <400> SEQUENCE: 10
234 Met Gly Glu Lys Glu Gly Gly Gly Gly Gly Asp Ala Ala Ala Ala Glu
235 1 5 10 15
236 Gly Gly Ala Gly Ala Ala Ala Ser Arg Ala Leu Gln Gln Cys Gly Gln
237 20 25 30
238 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
239 35 40 45
240 Thr Lys Cys Ala Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
241 50 55 60
242 Leu Glu Ala Lys Leu Val Arg Tyr Ile Cys Lys Gln Arg Gln Cys Lys
243 65 70 75 80
244 Leu Ser Val Ala Pro Gly Glu Arg Thr Pro Glu Leu Asn Ser Tyr Pro
245 85 90 95
246 Arg Phe Ser Asp Trp Leu Tyr Thr Phe Asn Val Arg Pro Glu Val Val
247 100 105 110
248 Gln Glu Ile Pro Arg Asp Leu Thr Leu Asp Ala Leu Leu Glu Met Asn
249 115 120 125
250 Glu Ala Lys Val Lys Glu Thr Leu Arg Arg Cys Gly Ala Ser Gly Asp
251 130 135 140
252 Glu Cys Gly Arg Leu Gln Tyr Ala Leu Thr Cys Leu Arg Lys Val Thr
253 145 150 155 160
254 Gly Leu Gly Gly Glu His Lys Glu Asp Ser Ser Trp Ser Ser Leu Asp
255 165 170 175
256 Ala Arg Arg Glu Ser Gly Ser Gly Pro Ser Thr Asp Thr Leu Ser Ala
257 180 185 190
258 Ala Ser Leu Pro Trp Pro Pro Gly Ser Ser Gln Leu Gly Arg Ala Gly
259 195 200 205
260 Asn Ser Ala Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala
261 210 215 220
262 Ser Asp Ser Pro Thr Pro Ser Phe Ser Glu Gly Leu Ser Asp Thr Cys
263 225 230 235 240
264 Ile Pro Leu His Ala Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser
265 245 250 255
266 Phe Ile Thr Pro Pro Thr Thr Pro Gln Leu Arg Arg His Thr Lys Leu
267 260 265 270
268 Lys Pro Pro Arg Thr Pro Pro Pro Ser Arg Lys Val Phe Gln Leu
269 275 280 285
270 Leu Pro Ser Phe Pro Thr Leu Thr Arg Arg Lys Ser His Glu Ser Gln
271 290 295 300
272 Leu Gly Asn Arg Ile Asp Asp Val Ser Ser Met Arg Phe Asp Leu Ser
273 305 310 315 320
274 His Gly Ser Pro Gln Met Val Arg Arg Asp Ile Gly Leu Ser Val Thr
275 325 330 335
276 His Arg Phe Ser Thr Lys Ser Trp Leu Ser Gln Val Cys His Val Cys
277 340 345 350

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VERIFICATION SUMMARY

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